

Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1-41. (cancelled)

42. (currently) A method of analyzing a sample of nucleic acids, the method comprising:

providing a plurality of probe molecules wherein the plurality comprises at least one probe molecule for each target nucleic acid sequence to be analyzed, the probe molecule comprising a region of sequence substantially complementary to a sequence in the target nucleic acid sequence and an internal capture tag sequence that is internal to a nucleic acid strand of said probe molecule;

contacting the plurality of probe molecules to a sample of nucleic acids under conditions that allow a set of probe molecules for which a complementary sequence is present among the nucleic acids of the sample, to hybridize to the respective complementary sequence;

cleaving the probes molecules of the set, wherein the cleavage is specific for the probe molecules that hybridize to nucleic acids of the sample and the cleavage positions the capture tag sequence of each cleaved probe molecule at a terminus of the cleaved probe molecule; and

detecting one or more of the cleaved probes by hybridizing the tag sequences to capture probes disposed on a substrate, thereby analyzing the sample of nucleic acids.

43. (previously added) The method of claim 42 wherein each probe molecule comprises a Type IIS restriction endonuclease recognition site positioned such that cleavage of the recognition site in a double stranded DNA into which the probe molecule is incorporated generates a nucleic acid having a single-stranded overhang that includes the tag sequence.

44. (previously presented) The method of claim 42 wherein the cleaving positions the capture tag sequence of each cleaved probe molecule in a single-stranded overhang.

45. (previously presented) The method of claim 44 wherein detecting comprises hybridizing capture tag sequences of the one or more cleaved probes to a plurality of capture probes.

46. (cancelled)

47. (previously presented) The method of claim 45 wherein each capture probe of the plurality of capture probes comprises a double stranded region and a single stranded region.

48. (previously presented) The method of claim 47 wherein the 3' end of the single stranded region is extendable.

49. (previously presented) The method of claim 47 wherein each capture probe of the plurality of capture probes forms a hairpin structure.

50. (previously presented) The method of claim 47 wherein each capture probe of the plurality of capture probes comprises a chemical moiety that allows for immobilization.

51. (previously presented) The method of claim 42 wherein detecting comprises hybridizing capture tag sequences of the one or more cleaved probes to a plurality of capture probes.

52. (previously presented) The method of claim 51 wherein the detecting comprises an enzyme mediated reaction.

53. (previously presented) The method of claim 52 wherein a derivative nucleic acid is a substrate or template for the enzyme mediated reaction.

54. (previously presented) The method of claim 52 wherein a capture probe is a substrate or template for the enzyme mediated reaction.

55. (previously presented) The method of claim 42 wherein the internal capture tag sequence of each probe molecule of the plurality of probe molecules is between 4 and 20 nucleotides in length.

56. (previously presented) The method of claim 42 wherein the internal capture tag sequence of each probe molecule of the plurality of probe molecules is between 4 and 8 nucleotides in length.

57. (previously presented) The method of claim 42 wherein the internal capture tag sequence of each probe molecule of the plurality of probe molecules is unique.

58. (previously presented) The method of claim 46 further comprising ligating capture tag sequences of the one or more cleaved probes to capture probes of the plurality of capture probes.

59. (new) The method of claim 42 further comprising, prior to the cleaving, extending probe molecules that hybridize to nucleic acids of the sample.

60. (new) The method of claim 42 wherein the cleaving comprises cleavage by a Type IIS restriction endonuclease.

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61. (new) The method of claim 42 wherein the cleaving comprises cleavage by a flap endonuclease.